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NON-INDEPENDENCE BETWEEN MARKERS ON HOMOEOLOGOUS CHROMOSOMES IN AN INTERSPECIFIC ALLOPOLYPLOID COTTON RILS POPULATION

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Cotton, as the world's main natural textile fibre, is the focus of many studies for genetic improvement of fibre quality. Two allotetraploid (AtDt genome, 2n=4X=52) species dominate world production: G. hirsutum (Gh) with medium fibre quality and G. barbadense (Gb) with high fibre quality, accounting for 95% / 3% of production respectively. A RIL population originating from a Gh-Gb cross is the base material of the CIRAD-Bayer CropScience-CSIRO ANR research project Cotton_RILs, aiming at the genetic and genomic dissection of cotton fibre quality for introgression of high fibre quality genes of Gb into Gh germplasm. Until now, classical breeding did not succeed at satisfactorily combining traits from both cotton species, in spite of high apparent synteny conservation between their chromosomes.

The fixed heterozygosity of allopolyploids is supposed to result in gene expression changes, or expression subfonctionalization, a partitioning of the ancestral expression domains among duplicate genes. It is hypothesized that allopolyploids should be subject to more genetic and epigenetic regulatory changes than autopolyploids.

We report here on evidence of interactions between markers on pairs of homoeologous chromosomes in the Gh-Gb RIL population studied (140 lines genotyped with 800 markers, assembled in a saturated map of 26 linkage groups). In five of the 13 homoeologous chromosome pairs (c12-c26, c6-c25, c11-c21, c3-c17 and c13-c18), markers from homoeologs displayed unexpectedly high linkage (LOD from 9 to 14). Such linkage was not observed between chromosomes from non-homoeologous pairs. The association concerns 1-3 markers from one chromosome against stretches of 5-8 or more markers on the homoeolog. Gametic disequilibrium (GD) has been assessed pairwise between all markers. Positive GD is highly dominant between markers of homoeologous chromosomes, but negative as well as positive GD are observed between markers of non-homoeologs, with uneven distribution. In positive GD, frequencies of Gh-Gb allelic combinations are very low, meanwhile in negative GD, there is uniform low frequency of Gb-Gb allelic combinations.

Diverse genetic and epigenetic mechanisms have been characterized in polyploid plants, including unequal expression of duplicate genes, segregation distortion and restricted recombination; in cotton, lesser retention of Gb alleles is a common feature of advanced-generation backcross or RIL interspecific populations. Our results support hypotheses of intergenomic incompatibility, with selection during inbreeding that favoured elimination of Gh-Gb allelic combinations that were too conflicting regarding the expression of duplicate genes.

Keywords: Cotton; interspecific RILs; intergenomic incompatibility; gametic disequilibrium